

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/560,303  
Source: FWP  
Date Processed by STIC: 12/20/05

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/560,303

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos        was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will  
                               prevent "wrapping."
  
- 2      Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers;  
     Numbering                use **space characters**, instead.
  
- 4      Non-ASCII             The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please**  
                               ensure your subsequent submission is saved in **ASCII** text.
  
- 5      Variable Length      Sequence(s)          contain n's or Xaa's representing more than one residue. **Per Sequence Rules,**  
                               each n or Xaa can only represent a single residue. Please present the **maximum** number of each  
                               residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                    sequences(s)                 . Normally, PatentIn would automatically generate this section from the  
                               previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                               the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**  
                               **Artificial or Unknown sequences.**
  
- 7      Skipped Sequences   Sequence(s)          missing. If intentional, please insert the following lines for **each** skipped sequence:  
     (OLD RULES)            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                               (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               This sequence is intentionally skipped  
  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences   Sequence(s)          missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
     (NEW RULES)            <210> sequence id number  
                               <400> sequence id number  
                               000
  
- 9      Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)            Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                               In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10     Invalid <213>        Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or  
     Response                scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or  
                               is Artificial Sequence
  
- 11     Use of <220>        Sequence(s)                  missing the <220> "Feature" and associated numeric identifiers and responses.  
                               Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or  
                               "Unknown." Please explain source of genetic material in <220> to <223> section.  
                               (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12     PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                    resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                               listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13     Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

DATE: 12/20/2005

PATENT APPLICATION: US/10/560,303

TIME: 11:21:39

Input Set : A:\601-1-131 PCT US NATL PHASE SEQUENCE LISTING.txt

Output Set: N:\CRF4\12202005\J560303.raw

4 <110> APPLICANT: Inouye, Masayori  
 5 Zhang, Junjie  
 6 Zhang, Yong Long  
 7 Qing, Guoliang  
 8 Suzuki, Motoo  
 10 <120> TITLE OF INVENTION: mRNA Interferases and Methods of Use Thereof  
 12 <130> FILE REFERENCE: University of Medicine & Dentistry of New Jersey (601-1-131PCT)  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/560,303  
 C--> 15 <141> CURRENT FILING DATE: 2005-12-12  
 17 <150> PRIOR APPLICATION NUMBER: 60/543,693  
 18 <151> PRIOR FILING DATE: 2004-02-11  
 20 <150> PRIOR APPLICATION NUMBER: 60/478,515  
 21 <151> PRIOR FILING DATE: 2003-06-13  
 23 <160> NUMBER OF SEQ ID NOS: 92  
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0

## ERRORED SEQUENCES

1411 <210> SEQ ID NO: 89  
 1412 <211> LENGTH: 17  
 1413 <212> TYPE: RNA  
 1414 <213> ORGANISM: Artificial Sequence  
 1416 <220> FEATURE:  
 1417 <223> OTHER INFORMATION: mRNA transcript  
 1419 <400> SEQUENCE: 89  
 E--> 1420 aatgatgaca ctggaag  
 1422 <210> SEQ ID NO: 90  
 1423 <211> LENGTH: 17  
 1424 <212> TYPE: RNA  
 1425 <213> ORGANISM: Artificial Sequence  
 1427 <220> FEATURE:  
 1428 <223> OTHER INFORMATION: mRNA transcript  
 1430 <400> SEQUENCE: 90  
 E--> 1431 gtcggtgaca ttgatgg  
 1433 <210> SEQ ID NO: 91  
 1434 <211> LENGTH: 17  
 1435 <212> TYPE: RNA  
 1436 <213> ORGANISM: Artificial Sequence  
 1438 <220> FEATURE:  
 1439 <223> OTHER INFORMATION: mRNA transcript  
 1441 <400> SEQUENCE: 91  
 E--> 1442 atctgaaca cgcagcc

pp 1-4  
 Does Not Comply  
 Corrected Diskette Needed

insufficient explanation - give source  
 of genetic material  
 (see item 11 on  
 Error Summary  
 sheet)  
 no t's allowed in an RNA sequence  
 (for a combined  
 DNA/RNA sequence,  
 use <212> DNA  
 and explain in  
 <220>-<223>  
 section)  
 same error

17  
 17  
 this error  
 appears  
 throughout  
 sequence listing

## RAW SEQUENCE LISTING

DATE: 12/20/2005

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TIME: 11:21:39

Input Set : A:\601-1-131 PCT US NATL PHASE SEQUENCE LISTING.txt

Output Set: N:\CRF4\12202005\J560303.raw

1444 &lt;210&gt; SEQ ID NO: 92

1445 &lt;211&gt; LENGTH: 17

1446 &lt;212&gt; TYPE: RNA

1447 &lt;213&gt; ORGANISM: Artificial Sequence

1449 &lt;220&gt; FEATURE:

1450 &lt;223&gt; OTHER INFORMATION: mRNA transcript

1452 &lt;400&gt; SEQUENCE: 92

E--> 1453 ~~ccgtttt~~aca ccgttga

17

*see p. 3 for more error*

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<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

need explanation  
(see p. 4)

<400> 14

agatctcgat cccgcaaatt aat

23

same error in sequence 30

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/560,303

DATE: 12/20/2005  
TIME: 11:21:40

Input Set : A:\601-1-131 PCT US NATL PHASE SEQUENCE LISTING.txt  
Output Set: N:\CRF4\12202005\J560303.raw

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:14,30

**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/10/560,303**

**DATE: 12/20/2005**

**TIME: 11:21:40**

**Input Set : A:\601-1-131 PCT US NATL PHASE SEQUENCE LISTING.txt**

**Output Set: N:\CRF4\12202005\J560303.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:240 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>  
ORGANISM:Artificial Sequence  
L:240 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>  
ORGANISM:Artificial Sequence  
L:240 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:240  
L:414 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:30, <213>  
ORGANISM:Artificial Sequence  
L:414 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:30, <213>  
ORGANISM:Artificial Sequence  
L:414 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:414  
L:1420 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:3  
L:1431 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:6  
L:1442 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2  
L:1453 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:7